

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/852,053

DATE: 08/07/2001

TIME: 13:32:58

Input Set : A:\Ma280248.app

Output Set: N:\CRF3\08072001\I852053.raw

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3 <110> APPLICANT: BERENS, STEPHAN
4     KALINOWSKI, JORN
5     PUHLER, ALFRED
7 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM STRAIN WITH
8     ENHANCED SECRETION ACTIVITY
10 <130> FILE REFERENCE: MAS/21123/280248
12 <140> CURRENT APPLICATION NUMBER: 09/852,053
13 <141> CURRENT FILING DATE: 2001-05-10
15 <150> PRIOR APPLICATION NUMBER: EPO 00110021.3
16 <151> PRIOR FILING DATE: 2000-05-12
18 <160> NUMBER OF SEQ ID NOS: 24
20 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 1960
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
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28 <221> NAME/KEY: misc_feature
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30 <223> OTHER INFORMATION: secD
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35 gtttatgctg tggtgctggt gacaggcgat cggtctgcca caccaaaatt gggattgat 180
36 ctgcaaggcg gaacccgagt gaccctcggt ccgcaggggc aggatccaac tcaggaccag 240
37 ctgaatcagg cagcaccat tctggaaaac cgtgtgaacg gcatgggctg ttcagggtga 300
38 agcgtggtcg ctgacggtaa cacgctggtg atcactgttc ccggggaaaa taccgcacag 360
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40 cccgatatga ccacgttgat gccagagctg gaagagatgg ccaacaggtg ggttgaatac 480
41 ggcgtcatca ccgaagagca ggcaaatgcc tccttgagg aaatgaacac cgctgttgca 540
42 tcgaccactg cggtggaagg cgaagaagca actgagccag aaccgcgcac cgtgtcggcg 600
43 acccctatgg atgagccagc caactccatt gaggcaaac agcgacgcca ggaaatcacg 660
44 gacatgctgc gcaccgaccg ccagtccacc gatccactg tccagatcgc tgcaagttct 720
45 ttgatgcagt gcaccactga tgagatggat cctttggccg gcaccgatga tccacgcctg 780
46 ccattggttg catgtgatcc agctgtaggt ggcgtgtatg tacttgatcc tgcacctttg 840
47 ctcaacggcg aaaccgatga ggaaaatggt gcgcgcctaa ccggtaatga gatcgatacc 900
48 aaccgtccca tcaccggtgg attcaacgcc cagtcgggcc agatggaaat cagctttgcc 960
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51 tcagcaaccc ctgtgggttc tgcaacatcc atcaccggtg acttactca aactgaagcc 1140
52 caagatctgg cgaacaacct gcgctacggt gcattgcccc tgagcttcgc aggtgaaaac 1200
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56 ggcccttcgt tactgtggg acgctggatc ggatattccc tagaccttgc tggatcgcc 1440
57 ggtttgatca tcggtatcgg taccaccgcc gactccttcg tgggtgtcta tgagcgcac 1500
58 aaggatgaga tccgtgaagg aagatccttt agatctgcag tacctcgtgc atgggaaagc 1560

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59 gccaaagcgca ccacgtcac aggcaacatg gtcactttgc tcggcgctat cgtgatttac 1620
60 ttgctcgcgg tcggcgaaagt caagggcttt gccttcaccc tgggtctgac caccgtattc 1680
61 gatctcgttg tcaccttctt gatcacggca ccactggta tcctggcatc acgcaaccca 1740
62 ttctttgcc agtcatcggg caacggcatg ggacgagtga tgaagctcgt tgaagaacgc 1800
63 cgcgccaaag gtgaattgga tgagcctgag tacctgaaaa agatccatgc caagaatgcg 1860
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76 <223> OTHER INFORMATION: secF
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91 accgtcgtgg tctttgacaa ggtcagagaa aacaccgaag gcttcgaagg cagccgcaga 780
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97 gccacccccc acaccaacgc cgacgcctcc gcgcacggca ccgaaagcga cactgacggt 1140
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101 acgacttcac gtggctgact tcagtcggat ttgccgtttt tatccagtga agtcggctca 1380
102 tgagaagttg agcacgcgaa gtcgtagggt gaggtctcgt aatctgcggt gtcgtagggt 1440
103 gagatgtcgc cgcttaagt tcgatttctc accttcgata cctcacgctc aatttcttat 1500
104 gttcgagacc gctaggaaaa gcacaaaaaa ccgactgaaa ttgagtttgg gaaattgagc 1560
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109 <211> LENGTH: 637
110 <212> TYPE: PRT
111 <213> ORGANISM: Corynebacterium glutamicum
113 <220> FEATURE:
114 <221> NAME/KEY: PROPEP

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115 <222> LOCATION: (1)..(637)  
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 122 Lys Arg Ala Ile Ala Leu Phe Val Leu Ile Val Val Gly Val Tyr Ala  
 123 20 25 30  
 125 Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro Lys Leu Gly Ile  
 126 35 40 45  
 128 Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro Gln Gly Gln Asp  
 129 50 55 60  
 131 Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg  
 132 65 70 75 80  
 134 Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val Ala Asp Gly Asn  
 135 85 90 95  
 137 Thr Leu Val Ile Thr Val Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser  
 138 100 105 110  
 140 Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val Gly Gln Ala Gly  
 141 115 120 125  
 143 Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu Glu Met Ala Asn  
 144 130 135 140  
 146 Arg Trp Val Glu Tyr Gly Val Ile Thr Glu Glu Gln Ala Asn Ala Ser  
 147 145 150 155 160  
 149 Leu Glu Glu Met Asn Thr Ala Val Ala Ser Thr Thr Ala Val Glu Gly  
 150 165 170 175  
 152 Glu Glu Ala Thr Glu Pro Glu Pro Val Thr Val Ser Ala Thr Pro Met  
 153 180 185 190  
 155 Asp Glu Pro Ala Asn Ser Ile Glu Ala Thr Gln Arg Arg Gln Glu Ile  
 156 195 200 205  
 158 Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp Pro Thr Val Gln  
 159 210 215 220  
 161 Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp Glu Met Asp Pro  
 162 225 230 235 240  
 164 Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val Ala Cys Asp Pro  
 165 245 250 255  
 167 Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro Leu Leu Asn Gly  
 168 260 265 270  
 170 Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly Asn Glu Ile Asp  
 171 275 280 285  
 173 Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln Ser Gly Gln Met  
 174 290 295 300  
 176 Glu Ile Ser Phe Ala Phe Lys Ser Gly Asp Gly Glu Glu Gly Ser Ala  
 177 305 310 315 320  
 179 Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln Gln Ile Ala Ile  
 180 325 330 335  
 182 Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile Gln Ser Ala Thr  
 183 340 345 350  
 185 Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe Thr Gln Thr Glu  
 186 355 360 365

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188 Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala Leu Pro Leu Ser
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191 Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr Thr Thr Val Pro
192 385      390      395      400
194 Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu Ile Ala Gly Ile
195      405      410      415
197 Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala Tyr Tyr Arg Val
198      420      425      430
200 Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala Gly Val Leu Val
201      435      440      445
203 Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly Tyr Ser Leu Asp
204      450      455      460
206 Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly Thr Thr Ala Asp
207 465      470      475      480
209 Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu Ile Arg Glu Gly
210      485      490      495
212 Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu Ser Ala Lys Arg
213      500      505      510
215 Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly Ala Ile Val Ile
216      515      520      525
218 Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala Phe Thr Leu Gly
219      530      535      540
221 Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu Ile Thr Ala Pro
222 545      550      555      560
224 Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala Lys Ser Ser Val
225      565      570      575
227 Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu Arg Arg Ala Asn
228      580      585      590
230 Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile His Ala Lys Asn
231      595      600      605
233 Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser Thr Asp Asn Ser
234      610      615      620
236 Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu Lys
237 625      630      635
240 <210> SEQ ID NO: 4
241 <211> LENGTH: 403
242 <212> TYPE: PRT
243 <213> ORGANISM: Corynebacterium glutamicum
244 <220> FEATURE:
245 <221> NAME/KEY: PROPEP
246 <222> LOCATION: (1)..(403)
247 <223> OTHER INFORMATION: secF
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254 Ala Lys Lys Arg Ser Trp Phe Asn Ser Leu Tyr Thr Gly Asp Gly Gly
255      20      25      30
257 Ile Asp Phe Ile Ala Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile
258      35      40      45

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260 Leu Leu Val Ile Ser Ile Leu Phe Ile Ala Ile Arg Gly Phe Ser Leu
261      50      55      60
263 Ser Ile Asp Phe Gln Gly Gly Thr Lys Met Ser Met Pro Ala Ser Asp
264      65      70      75      80
266 Tyr Ser Thr Glu Gln Val Glu Glu Thr Phe Thr Glu Ala Thr Gly Ile
267      85      90      95
269 Thr Pro Glu Ile Val Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu
270      100      105      110
272 Glu Ile Tyr Ser Glu Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg
273      115      120      125
275 Leu Ala Ile Tyr Glu Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro
276      130      135      140
278 Ser Pro Asp Ala Ile Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser
279      145      150      155      160
281 Thr Ile Thr Gln Arg Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile
282      165      170      175
284 Ala Ala Ile Tyr Ile Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala
285      180      185      190
287 Ala Met Ala Ala Leu Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr
288      195      200      205
290 Ala Val Ile Gly Leu Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu
291      210      215      220
293 Thr Val Leu Thr Phe Ser Ile Tyr Asp Thr Val Val Phe Asp Lys
294      225      230      235      240
296 Val Arg Glu Asn Thr Glu Gly Phe Glu Gly Ser Arg Arg Arg Thr Tyr
297      245      250      255
299 Ala Glu Gln Ala Asn Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile
300      260      265      270
302 Ser Thr Thr Ile Ile Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val
303      275      280      285
305 Ala Val Trp Met Met Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile
306      290      295      300
308 Gln Leu Ile Gly Val Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala
309      305      310      315      320
311 Thr Pro Leu Leu Val Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala
312      325      330      335
314 His Thr Ala Ser Val Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile
315      340      345      350
317 Asp Ala Thr Pro His Thr Asn Ala Asp Ala Ser Ala His Gly Thr Glu
318      355      360      365
320 Ser Asp Thr Asp Gly Val Thr Pro Glu Ala Pro Ala Lys Arg Thr Val
321      370      375      380
323 Ser Lys Pro Ile Val Asp Asp His Arg Ser Ser Gly Thr Trp Arg Pro
324      385      390      395      400
326 Gly Arg Ser
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330 <211> LENGTH: 20
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

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